Amendments

Amendments to the Claims

Please amend the claims as shown below in the List of Claims

List of Claims

1-12. (Canceled).

13. (Currently Amended) A process for the production of an L-amino acid chosen from the group consisting of L-threonine, L-isoleucine, L-valine, L-methionine, L-homoserine and L-lysine comprising:

a) fermenting a bacterium comprising an overexpressed ~~endogenous~~ DNA sequence encoding the galactose-proton symporter protein in said bacterium, in a fermentation medium under conditions suitable for the production of said L-amino acid, wherein:

i) said bacterium is of an Enterobacteriaceae family;

ii) said galactose-proton symporter protein comprises the amino acid sequence of SEQ ID NO:4 and is encoded by the nucleotide sequence of residues 33-1427 of SEQ ID NO:3;

iii) said L-amino acid is produced from glucose, saccharose, lactose, fructose, molasses, starch, cellulose or from glycerine and ethanol;

iv) said overexpression is achieved by increasing the copy number of said DNA or by ~~operably linking said DNA to a promoter~~ changing a promoter normally found in a galP gene; and

b) allowing said L-amino acid to become enriched in said bacteria or said fermentation medium.

14. (Previously Presented) The process of claim 13, wherein said galactose-proton symporter protein consists of the amino acid sequence of SEQ ID NO:4.

15. (Currently Amended) The process of claim 14, wherein said DNA sequence encoding the galactose-proton symporter protein consists of the nucleotide sequence of residues 33-1427 of SEQ ID NO:3.

16. (Currently Amended) The process of claim 13, wherein said DNA sequence encoding the galactose-proton symporter protein consists of the nucleotide sequence of residues 33-1427 of SEQ ID NO:3.

17. (Previously Presented) The process of claim 13, wherein overexpression is achieved by increasing the copy number of said DNA.

18. (Previously Presented) The process of claim 13, wherein said L-amino acid is L-threonine.

19. (Previously Presented) The process of any one of claims 13-16, further comprising isolating said L-amino acid along with some or all of the constituents of said fermentation medium and/or the biomass in said fermentation medium.

20. (Previously presented) The process of claim 19, wherein said L-amino acid is L-threonine.

21. (Currently Amended) The process of claim 13, wherein said microorganism overexpresses one or more genes selected from the group consisting of:

a) ~~the~~ a thrABC operon coding for aspartate kinase, homoserine dehydrogenase, homoserine kinase and threonine synthase;

b) ~~the~~ a pyc gene coding for pyruvate carboxylase;

c) ~~the~~ a pps gene coding for phosphoenolpyruvate synthase;

d) ~~the~~ a ppc gene coding for phosphoenolpyruvate carboxylase;

e) ~~the~~ pntA and pntB genes coding for transhydrogenase,

f) ~~the~~ a rhtB gene which imparts homoserine resistance;

g) ~~the~~ a mqo gene coding for malate:quinone oxidoreductase;

h) ~~the~~ a rhtC gene which imparts threonine resistance;

i) the thrE gene coding for threonine export protein;

j) ~~the~~ a gdhA gene coding for glutamate dehydrogenase;

k) ~~the~~ a glk gene coding for glucokinase;

l) ~~the~~ a hns gene coding for DNA binding protein HLP-II;

m) ~~the~~ a pgm gene coding for phosphoglucomutase;

n) ~~the~~ a fba gene coding for fructose biphosphate aldolase;

o) ~~the~~ a ptsH gene coding for phosphohistidine protein hexose phosphotransferase;

p) ~~the~~ a ptsI gene coding for enzyme I in the phosphotransferase system;

q) ~~the~~ a crr gene coding for the glucose-specific IIA component;

r) ~~the~~ a ptsG gene coding for the glucose-specific IIBC component;

s) ~~the~~ a lrp gene coding for a regulator in the leucine regulon;

t) ~~the~~ a csrA gene coding for the global regulator Csr;

u) ~~the~~ a fadR gene coding for a regulator in the fad regulon;

v) ~~the~~ a iclR gene coding for a regulator in central intermediary metabolism;

w) ~~the~~ a mopB gene coding for the 10 KDa chaperone;

x) ~~the~~ a ahpC gene coding for the small sub-unit of alkyl hydroperoxide reductase;

y) ~~the~~ a ahpF gene coding for the large sub-unit of alkyl hydroperoxide reductase;

z) ~~the~~ a cysK gene coding for cysteine synthase A;

aa) ~~the~~ a cysB gene coding for the regulator in the cys regulon;

bb) ~~the~~ a cysJ gene coding for the flavoprotein in NADPH sulfite reductase;

cc) ~~the~~ a cysI gene coding for haemoprotein in NADPH sulfite reductase;

dd) ~~the~~ a cysH gene coding for adenylylsulfate reductase;

ee) ~~the~~ a phoB gene coding for the positive regulator PhoB in the pho regulon;

ff) ~~the~~ a phoR gene coding for the sensor protein in the pho regulon;

gg) ~~the~~ a phoE gene coding for protein E in the outer cell membrane;

hh) ~~the~~ a pykF gene coding for the pyruvate kinase I stimulated by fructose;

ii) ~~the~~ a pfkB gene coding for 6-phosphofructokinase II;

jj) ~~the~~ a malE gene coding for periplasmatic binding protein in maltose transport;

kk) ~~the~~ a sodA gene coding for superoxidedismutase;

ll) ~~the~~ a rseA gene coding for a membrane protein with anti-sigmaE activity;

mm) ~~the~~ a rseC gene coding for a global regulator in the sigmaE factor;

nn) ~~the~~ a sucA gene coding for the decarboxylase sub-unit of 2-ketoglutarate dehydrogenase;

oo) ~~the~~ a sucB gene coding for the dihydrolipoyl-transsuccinase E2 subunit of 2-ketoglutarate dehydrogenase;

pp) ~~the~~ a sucC gene coding for the β-subunit of succinyl-CoA synthetase;

qq) ~~the~~ a sucD gene coding for the α-subunit in succinyl-CoA synthetase;

rr) ~~the~~ a adk gene coding for adenylate kinase;

ss) ~~the~~ a hdeA gene coding for a periplasmatic protein with a chaperonin-like function;

tt) ~~the~~ a hdeB gene coding for a periplasmatic protein with a chaperonin-like function;

uu) ~~the~~ a icd gene coding for isocitrate dehydrogenase;

vv) ~~the~~ a mglB gene coding for periplasmatic, galactose-binding transport protein;

ww) ~~the~~ a lpd gene coding for dihydrolipoamide dehydrogenase;

xx) ~~the~~ a aceE gene coding for the E1 component of pyruvate dehydrogenase complex;

yy) ~~the~~ a aceF gene coding for the E2 component of pyruvate dehydrogenase complex;

zz) ~~the~~ a pepB gene coding for aminopeptidase B;

aaa) ~~the~~ a aldH gene coding for aldehyde dehydrogenase;

bbb) ~~the~~ a bfr gene coding for the iron storage homoprotein;

ccc) ~~the~~ a udp gene coding for uridine phosphorylase; and

ddd) ~~the~~ a rseB gene coding for the regulator of sigmaE factor activity;

wherein said overexpression is achieved by one or more methods selected from the group consisting of increasing copy number, using a strong promoter, and mutating the ribosome binding site.

22. (Currently Amended) The process of claim 13, wherein at least one gene in said microorganism is ~~attenuated~~ deleted, said gene being selected from the group consisting of:

a) ~~the~~ a tdh gene coding for threonine dehydrogenase;

b) ~~the~~ a mdh gene coding for malate dehydrogenase;

c) ~~the~~ a gene product of the open reading frame (ORF) yjfA;

d) ~~the~~ a gene product of the open reading frame (ORF) ytfP;

e) ~~the~~ a pckA gene coding for the enzyme phosphoenol-pyruvate carboxykinase;

f) ~~the~~ a poxB gene coding for pyruvate oxidase;

g) ~~the~~ a aceA gene coding for isocitrate lyase;

~~h) the a dgsA gene coding for the DgsA regulator in the phosphotransferase system;~~

~~i~~ h) ~~the~~ a fruR gene coding for fructose repressor;

~~j~~ i) ~~the~~ a rpoS gene coding for the sigma^{38}-Factor;

~~k~~ j) ~~the~~ a aspA gene coding for aspartate ammonium lyase; and

~~l~~ k) ~~the~~ a aceB gene coding for malate synthase A gene.

23. (Currently amended) A process for the production of an L-amino acid chosen from the group consisting of L-threonine, L-isoleucine, L-valine, L-methionine, L-homoserine and L-lysine comprising:

a) fermenting a bacterium comprising an overexpressed ~~endogenous~~ DNA sequence encoding the galactose-proton symporter protein in said bacterium,

in a fermentation medium under conditions suitable for the production of said L-amino acid, wherein:

i) said bacterium is of an Enterobacteriaceae family and ~~transports glucose by a PEP-dependent phosphotransferase (PTS) pathway~~ comprises PTS enzymes;

ii) said galactose-proton symporter protein comprises the amino acid sequence of SEQ ID NO:4;

iii) said L-amino acid is produced from glucose, saccharose, lactose, fructose, molasses, starch, cellulose or from glycerine and ethanol;

iv) said overexpression is achieved by increasing the copy number of said DNA or by ~~operably linking said DNA to a promoter~~ changing a promoter normally found in a galP gene; and

b) allowing said L-amino acid to become enriched in said bacteria or said fermentation medium.

24. (Previously presented) The process of claim 23, further comprising isolating said L-amino acid along with some or all of the constituents of said fermentation medium and/or the biomass in said fermentation medium.

25. (Previously Presented) The process of claim 24, wherein said bacterium is selected from the group consisting of: Escherichia coli H4581; Escherichia coli VNIIgenetika MG442; Escherichia coli VNIIgenetika M1; Escherichia coli VNIIgenetika 472T23; Escherichia coli BKIIM B-3996; Escherichia coli kat 13; and Escherichia coli KCCM-10132.

26. (Previously presented) The process of claim 25, wherein said L-amino acid is L-threonine.